



SEQUENCE LISTING

<110> Korman, Alan  
Halk, Edward L.  
Lonberg, Nils  
Medarex, Inc.

<120> Human CTLA-4 Antibodies and Their Uses

<130> 014643-010510US

<140> US 09/644,668

<141> 2000-08-24

<150> US 60/150,452

<151> 1999-08-24

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 3159

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cloning vector  
pGPLk

<400> 1

```

aattagcggc cgctgtcgac aagcttcgaa ttcagtatcg atgtggggta cctactgtcc 60
cgggattgcy gatccgcgat gatctcggtg atcctcgagt gcggccgcag tatgcaaaaa 120
aaagcccgct cattaggcgg gctcttgga gaacatatcc atcgcgctccg ccatctccag 180
cagccgcacg cggcgcatct cgggcagcgt tgggtcctgg ccacgggtgc gcatgatcgt 240
gctcctgtcg ttgaggaccc ggctaggctg gcgggggtgc cttactgggt agcagaatga 300
atcaccgata cgcgagcgaa cgtgaagcga ctgctgctgc aaaacgtctg cgacctgagc 360
aacaacatga atggtcttcg gtttcctgtt ttcgtaaagt ctggaaacgc ggaagtcagc 420
gccctgcacc attatgttcc ggatctgcat cgcaggatgc tgctggctac cctgtggaac 480
acctacatct gtattaacga agcgttgga ttgacctga gtgatttttc tctgggtccc 540
ccgcatccat accgccagtt gtttacctc acaacgttcc agtaaccggg catgttcata 600
atcagtaacc cgtatcgtga gcatcctctc tcgtttcatt ggtatcatta cccccatgaa 660
cagaaattcc cccttacacg gaggcacaa gtgaccaaac agggaaaaac cgcccttaac 720
atggcccgct ttatcagaag ccagacatta acgcttctgg agaaactcaa cgagctggac 780
gcggatgaac aggcagacat ctgtgaatcg cttaacgacc acgctgatga gctttaccgc 840
agctgcctcg cgcgtttcgg tgatgacggt gaaaacctct gacacatgca gctcccggag 900
acggtcacag cttgtctgta agcggatgcc gggagcagac aagcccgta gggcgctca 960
gcgggtgttg gcgggtgtcg gggcgagcc atgaccagc cacgtagcga tagcggagt 1020
tatactggct taactatgcy gcatcagagc agattgtact gagagtgcac catatgcggt 1080
gtgaaatacc gcacagatgc gtaaggagaa aataccgcat caggcgctct tccgcttcc 1140
cgctcactga ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca gctcactcaa 1200
aggcggtaat acggttatcc acagaatcag gggataacgc agggaaagaa atgtgagcaa 1260
aaggccagca aaaggccagg aaccgtaaaa aggcccggtt gctggcggtt ttccataggc 1320
tccgcccccc tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg cgaaaccoga 1380
caggactata aagataccag gcgtttcccc cctcgtagcgc tctcctgttc 1440
cgaccctgcc gcttacggga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt 1500
ctcatagctc acgctgtagg tatctcagtt cgggtgtaggt cgttcgctcc aagctgggct 1560
gtgtgcacga acccccgtt cagcccagac gctgcgcctt atccggtaac tatcgtcttg 1620
agtccaaccc ggtaagacac gacttatcgc cactggcagc agccaggcgc gccttggcct 1680
aagaggccac tggtaacagg attagcagag cgaggtatgt aggcgggtgt acagagttct 1740
tgaagtgggt gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc 1800

```

TECH CENTER 1600/2900

JAN 15 2002

RECEIVED

TECH

JA

RF

Bw

1470

tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	atccggcaaa	caaaccaccg	1860
ctggtagcgg	tgggtttttt	gtttgcaagc	agcagattac	gcgcagaaaa	aaaggatctc	1920
aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	gtggaacgaa	aactcacgtt	1980
aagggatttt	ggatcatgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	ttaaattaaa	2040
aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac	ttgggtctgac	agttaccaat	2100
gcttaatcag	tgaggcacct	atctcagcga	tctgtctatt	tcggtcatcc	atagttgcct	2160
gactccccgt	cgtgtagata	actacgatac	gggagggtt	accatctggc	cccagtgtctg	2220
caatgatacc	gcgagacca	cgctcaccgg	ctccagattt	atcagcaata	aaccagccag	2280
ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc	cgctccatc	cagtctatta	2340
attgttgccg	ggaagctaga	gtaagtagtt	cgccagttaa	tagtttgccg	aacgttggtg	2400
ccattgctgc	aggcatcgtg	gtgtcacgct	cgtcgttttg	tatggcttca	ttcagctccg	2460
gttcccaacg	atcaaggcga	gttacatgat	ccccatggt	gtgcaaaaaa	gcggttagct	2520
ccttcggtcc	tccgatcggt	gtcagaagta	agttggccgc	agtgttatca	ctcatgggta	2580
tggcagcact	gcataattct	cttactgtca	tgccatccgt	aagatgcttt	tctgtgactg	2640
gtgagtactc	aaccaagtca	ttctgagaat	agtgtatgcg	gcgaccgagt	tgctcttgcc	2700
cggcgtcaac	acgggataat	accgcgccac	atagcagaac	tttaaaagtg	ctcatcattg	2760
gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	gctgttgaga	tccagttcga	2820
tgtaaccac	tctgtcaccc	aactgatctt	cagcatcttt	tactttcacc	agcgtttctg	2880
ggtgagcaaa	aacaggaagg	caaaatgccg	caaaaaagg	aataagggcg	acacggaaat	2940
gttgaatact	catactcttc	ctttttcaat	attattgaag	catttatcag	ggttattgtc	3000
tcattgagcgg	atacatattt	gaatgtattt	agaaaaataa	acaaatagg	gttccgcgca	3060
catttccccg	aaaagtgcc	cctgacgtct	aagaaaccat	tattatcatg	acattaacct	3120
ataaaaaatag	gcgtatcacg	aggccctttc	gtcttcaag			3159

<210> 2

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<223> preliminary sequence for heavy chain fragment  
10D1.3

<400> 2

tgggggaggc	gtgggtccagc	ctgggagggtc	cctgagactc	tctgtgagc	cctctggatt	60
caccttcagt	agctatacta	tgcactgggt	ccgccagggt	ccaggcaagg	ggctggagtg	120
ggtgacattt	atatcatatg	atggaaacaa	taaatactac	gcagactccg	tgaagggccg	180
attcaccatc	tccagagaca	attccaagaa	cacgctgtat	ctgcaaatga	acagcctgag	240
agctgaggac	acggctatat	attactgtgc	gaggaccggc	tggtggggc	cctttgacta	300
ctggggccag	ggaaccctgg	tcaccgtctc	ctcagcctcc	accaagggc		349

<210> 3

<211> 321

<212> DNA

<213> Homo sapiens

<220>

<223> preliminary sequence for light chain fragment  
10D1.3

<400> 3

ctccaggcac	cctgtctttg	tctccagggg	aaagagccac	cctctcctgc	agggccagtc	60
agagtgttgg	cagcagctac	ttagcctggg	accagcagaa	acctggccag	gctcccaggc	120
tctcatcta	tggtgcattc	agcaggggcca	ctggcatccc	agacagggtc	agtggcagtg	180
ggtctgggac	agacttcact	ctcaccatca	gcagactgga	gcctgaagat	tttgcaagtgt	240
attactgtca	gcagtatggg	agctcaccgt	ggacgttcgg	ccaagggacc	aaggtggaaa	300
tcaaacgaac	tgtggctgca	c				321

<210> 4  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Vk A-27 germline sequence

<400> 4  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacc 287

<210> 5  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 Vk A-27 germline

<400> 5  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser  
 85 90 95

<210> 6  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> light chain variable region (Vk), 10D1 from Vk  
 A-27

<400> 6  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300  
 caagggacca aggtggaaat caaac 325

<210> 7  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 10D1 from Vk A-27

<400> 7  
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
 20 25 30  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95  
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 8  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> light chain variable region (Vk) 4B6 from Vk A-27

<400> 8  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttagc agcagcttct tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtga ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300  
 caagggacca aggtggaaat caaac 325

<210> 9  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 4B6 from Vk A-27

<400> 9

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30  
 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45  
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60  
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80  
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95  
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 10  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Vk L-15 germline sequence

<400> 10  
 gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgct gggcgagtca gggatttagc agctggtag cctgggtatca gcagaaacca 120  
 gagaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
 gaagattttg caacttatta ctgccaaacag tataatagtt accctcc 287

<210> 11  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain variable region predicted sequence for  
 Vk L-15 germline

<400> 11  
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr  
85 90

<210> 12  
<211> 322  
<212> DNA  
<213> Homo sapiens

<220>  
<223> light chain variable region Vk 1E2 from Vk L-15

<400> 12  
gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgtc gggcgagtc gggatttagc agctggtag cctggtagc gcagaaacca 120  
gagaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240  
gaagattttg caacttatta ctgccaacag tataatagtt accctccgac gttcggccaa 300  
gggaccaagg tggaaatcaa ac 322

<210> 13  
<211> 107  
<212> PRT  
<213> Homo sapiens

<220>  
<223> light chain variable region predicted sequence for  
1E2 from Vk L-15

<400> 13  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
35 40 45  
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Pro  
85 90 95  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 14  
<211> 294  
<212> DNA  
<213> Homo sapiens

<220>

<223> VH 3-30.3 germline sequence

<400> 14

```
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agctgaggac acggctgtgt attactgtgc gaga      294
```

<210> 15

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain variable region predicted sequence for  
VH 3-30.3 germline

<400> 15

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
  1              5              10              15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
      20              25              30
```

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35              40              45
```

```
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
      50              55              60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65              70              75              80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85              90              95
```

Ala Arg

<210> 16

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<223> heavy chain variable region VH 10D1 from VH 3-30.3

<400> 16

```
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300
tggctggggc cctttgacta ctggggccag ggaacctggg tcaccgtctc ctcag      355
```

<210> 17

<211> 118

B20

<212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain variable region predicted sequence for  
 10D1 from VH 3-30.3

<400> 17  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95  
 Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser  
 115

<210> 18  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> heavy chain variable region VH 4B6 from VH 3-30.3

<400> 18  
 cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggagggtc cctgagactc 60  
 tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120  
 ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaagcaa taaacactac 180  
 gcagactccg tgaagggccg attcaccgtc tccagagaca attccaagaa cacgctgtat 240  
 ctgcaaatac acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300  
 tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctacg 355

<210> 19  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain variable region predicted sequence for  
 4B6 from VH 3-30.3

<400> 19  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg



B<sup>20</sup>

<220>  
<223> VH 3-33 germline sequence

```
<210> 21
<211> 98
<212> PRT
<213> Homo sapiens
```

<400> 21  
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg

<210> 22  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> heavy chain variable region VH 1E2 from VH 3-33

<400> 22  
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggagggtc cctgagactc 60  
 tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccagggt 120  
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180  
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
 ctgcaaataa acagcctgag agccgaggac acggctgtgt tttactgtgc gagagctccc 300  
 aattatattg gtgcttttga tgtctggggc caagggacaa tggtcaccgt ctcttcag 358

<210> 23  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain variable region predicted sequence for  
 1E2 from VH 3-33

<400> 23  
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Phe Tyr Cys  
 85 90 95  
 Ala Arg Ala Pro Asn Tyr Ile Gly Ala Phe Asp Val Trp Gly Gln Gly  
 100 105 110  
 Thr Met Val Thr Val Ser Ser  
 115

<210> 24  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain CDR1 (HuMab 10D1)

<400> 24  
 Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala  
       1                  5                  10

<210> 25  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain CDR1 (HuMab 4B6)

<400> 25  
 Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala  
       1                  5                  10

<210> 26  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain CDR1 (HuMab 1E2)

<400> 26  
 Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala  
       1                  5                  10

<210> 27  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain CDR1 (HuMab 10D1, 4B6)

<400> 27  
 Ser Tyr Thr Met His  
       1                  5

<210> 28  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain CDR1 (HuMab 1E2)

Bio

<400> 28  
Ser Tyr Gly Met His  
1 5

<210> 29  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<223> light chain CDR2 (HuMab 10D1)

<400> 29  
Gly Ala Phe Ser Arg Ala Thr  
1 5

<210> 30  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<223> light chain CDR2 (HuMab 4B6)

<400> 30  
Gly Ala Ser Ser Arg Ala Thr  
1 5

<210> 31  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<223> light chain CDR2 (HuMab 1E2)

<400> 31  
Ala Ala Ser Ser Leu Gln Ser  
1 5

<210> 32  
<211> 17  
<212> PRT  
<213> Homo sapiens

<220>  
<223> heavy chain CDR2 (HuMab 10D1)

<400> 32  
Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 33  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain CDR2 (HuMab 4B6)

<400> 33  
 Phe Ile Ser Tyr Asp Gly Ser Asn Lys His Tyr Ala Asp Ser Val Lys  
           1                  5                  10                  15

Gly

<210> 34  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> heavy chain CDR2 (HuMab 1E2)

<400> 34  
 Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
           1                  5                  10                  15

Gly

<210> 35  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain CDR3 (HuMab 10D1, 4B6)

<400> 35  
 Gln Gln Tyr Gly Ser Ser Pro Trp Thr  
           1                  5

<210> 36  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> light chain CDR3 (HuMab 1E2)

<400> 36  
 Gln Gln Tyr Asn Ser Tyr Pro Pro Thr  
           1                  5

<210> 37  
 <211> 9  
 <212> PRT

<213> Homo sapiens

<220>

<223> heavy chain CDR3 (HuMab 10D1, 4B6)

<400> 37

Thr Gly Trp Leu Gly Pro Phe Asp Tyr

1

5

<210> 38

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> heavy chain CDR3 (MuMab 1E2)

<400> 38

Ala Pro Asn Tyr Ile Gly Ala Phe Asp Val

1

5

10

<210> 39

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:kappa light  
chain plasmid pCK7-96 (partial)

<400> 39

```
aggagaatga ataaataaag tgaatctttg cacctgtggt ttctctcttt cctcaattta 60
ataattatta tctgttggtt accaactact caatttctct tataagggac taaatatgta 120
gtcatcctaa ggcgcataac catttataaa aatcatcctt cattctattt taccctatca 180
tcctctgcaa gacagtcctc cctcaaacc cacaagcctt tgctctcaca gtcccctggg 240
ccatggatcc tcacatccca atccgcggcc gcaattcgta atcatggta tagctgtttc 300
ctgtgtgaaa ttgttatccg ctcaacaatt cacacaacat acgagccgga agcataaagt 360
gtaaagcctg gggcgcctaa tgagtgcctt aactcacatt aattgcgttg cgctcactgc 420
ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg 480
ggagaggcgg tttgctgatt gggcgc
```

506

<210> 40

<211> 4723

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:gamma heavy  
chain plasmid pCG-96

<400> 40

```
gaactcgagc agctgaagct ttctggggca ggccaggcct gaccttggct ttggggcagg 60
gagggggcta aggtgaggca ggtggcgcca gccagggtgca caccatgctc ccatgagccc 120
agacactgga cgctgaacct cgcgacagt taagaaccca ggggcctctg cgccctgggc 180
ccagctctgt cccacaccgc ggtcacatgg caccacctct cttgcagcct ccaccaaggg 240
cccatcggtc ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct 300
gggctgcctg gtcaaggact acttccccga accgggtgacg gtgtcgtgga actcaggcgc 360
cctgaccagc ggcgtgcaca cttccccggc tgtcctacag tcctcaggac tctactccct 420
```

```

cgaaaactct caaggatctt accgctgttg agatccagtt cgatgtaacc cactcgtgca 4140
cccaactgat cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga 4200
aggcaaaatg ccgcaaaaaa gggaataagg gcgacacgga aatgttgaat actcatactc 4260
ttcctttttc aatattattg aagcatttat cagggttatt gtctcatgag cggatacata 4320
tttgaatgta tttagaaaaa taaacaaata ggggttccgc gcacatttcc ccgaaaagtg 4380
ccacctgacg tctaagaaac cattattatc atgacattaa cctataaaaa taggcgtatc 4440
acgaggccct ttcgtctcgc gcgtttcggg gatgacgggtg aaaacctctg acacatgcag 4500
ctcccggaga cggtcacagc ttgtctgtaa gcggatgccg ggagcagaca agcccgtcag 4560
ggcgcgtcag cgggtgttgg cgggtgtcgg ggctggctta actatgcggc atcagagcag 4620
attgtactga gagtgcacca tatggacata ttgtcgttag aacgcggcta caattaatac 4680
ataaccttat gtatcatata catacgattt aggtgacact ata 4723

```

<210> 41

<211> 4694

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:gamma4 heavy  
chain plasmid pG4HE

<400> 41

```

gaactcgagc agctgaagct ttctggggca ggccgggcct gactttggct gggggcaggg 60
aggggggctaa ggtgacgcag gtggcgccag ccaggtgcac acccaatgcc catgagccca 120
gacactggag cctgcatgga ccacgcgga tagacaagaa ccgagggggc tctgcgccct 180
gggcccagct ctgtcccaca ccgcggtcac atggcaccac ctctcttgca gcttccacca 240
agggcccatc cgtcttcccc ctggcgccct gctccaggag cacctccgag agcacagccg 300
ccctgggctg cctggtcaag gactacttcc ccgaaccggg gacggtgtcg tggaaactcag 360
gcgcctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca ggactctact 420
ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacgaagacc tacacctgca 480
acgtagatca caagcccagc aacaccaagg tggacaagag agttggtgag agggcagcac 540
agggaggggc ggtgctgtgt ggaagccctc ctgcctggac gcaccccggc 600
tgtgcagccc cagcccaggg cagcaaggca tgccccatct gtctcctcac ccggaggcct 660
ctgaccaccc cactcatgct cagggagagg gtcttctgga tttttccacc aggctccggg 720
cagccacagg ctggatgccc ctaccccagg ccctgcgcac acagggggcag gtgctgcgct 780
cagacctgcc aagagccata tccgggagga ccctgcccct gacctaaagg cccccaaaag 840
gcaaaactct ccactccctc agctcagaca ccttctctcc tcccagatct gagtaactcc 900
caatcttctc tctgcagagt ccaaatatgg tcccccatgc ccatcatgcc caggtgaaggc 960
aaccagggcc ctgcctcca gctcaaggcg ctacaggtgc cctagagtag cctgcatcca 1020
gggacaggcc ccagccgggt gctgacgcat ccactccat ctcttctca gcacctgagt 1080
tcttgggggg accatcagtc ttctgttcc ccccaaaaacc caaggacact ctcatgatct 1140
cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc 1200
agttcaactg gtacgtggat ggctggagg tgcataatgc caagacaaag ccgcgggagg 1260
agcagttcaa cagcacgtac cgtgtggtca gcgtctcac cgtcctgcac caggactggc 1320
tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga 1380
aaacctctc caaagccaaa ggtgggaccc acggggtgcg agggccacat ggacagagg 1440
cagctcggcc caccctctgc cctgggagtg accgctgtgc caacctctgt ccctacaggg 1500
cagccccgag agccacagggt gtacacctg ccccatccc aggaggagat gaccaagaac 1560
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtg 1620
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1680
ggctccttct tctctacag caggetaacc gtggacaaga gcaggtggca ggaggggaat 1740
gtcttctcat gctcgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 1800
tctctgtctc tgggtaaatg agtgccaggg ccggcaagcc ccgctctccc gggctctcgg 1860
ggctgcgcga gctgcttgg cagtgacccc gtctacatac ttcccaggca cccagcatgg 1920
aaataaagca cccaccactg cctgggccc ctgtgagact gtgatggttc tttccacggg 1980
tcaggccgag tctgaggcct gagtgcacatg agggaggcag agcgggtccc actgtcccca 2040
cactggccca ggctgtgcag gtgtgcctgg gccacctagg gtggggctca gccaggggct 2100
gccctcggca ggggtggggga tttgccagcg tggcctccc tccagcagca gctgccctgg 2160
gctgggccac gggaagccct agggagccct ggggacagac acacagcccc tgctctgta 2220
ggagactgtc ctgtcctgtg agcgcctgtg cctccgaccc cccatgcccc ctccggggga 2280

```

Bio

tccccgggta ccgagctcga attcatcgat gatatcagat ctgccgggtct ccctatagtg 2340  
 agtcgtatta atttcgataa gccagggttaa cctgcattaa tgaatcggcc aacgcgcggg 2400  
 gagaggcggg ttgcgtattg ggcgctcttc cgcttcctcg ctcaactgact cgctgcgctc 2460  
 ggtcgttcgg ctgcggcgag cgggtatcagc tcaactcaaag gcggtaatac gggtatccac 2520  
 agaatcaggg gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa aggccaggaa 2580  
 ccgtaaaaag gccgcgttgc tggcggtttt ccataggctc cgccccctg acgagcatca 2640  
 caaaaatcga cgctcaagtc agaggtggcg aaacccgaca ggactataaa gataccaggc 2700  
 gtttccccct ggaagctccc tcgtgcgctc tcctgttccg accctgccgc ttaccggata 2760  
 cctgtccgcc tttctccctt cgggaagcgt ggcgctttct caatgctcac gctgtaggta 2820  
 tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt gtgcacgaac ccccggttca 2880  
 gccccagcgc tgcgccttat ccggttaacta tcgtcttgag tccaacccgg taagacacga 2940  
 cttatcgcca ctggcagcag ccactggtaa caggattagc agagcgaggt atgtaggcgg 3000  
 tgctacagag ttcttgaagt ggtggcctaa ctacggctac actagaagga cagtatttgg 3060  
 tatctgcgct ctgctgaagc cagttacctt cggaaaaaga gttggtagct cttgatccgg 3120  
 caaacaaaacc accgctggta gcggtggttt ttttgtttgc aagcagcaga ttacgcgcag 3180  
 aaaaaaagga tctcaagaag atcctttgat cttttctacg gggctctgacg ctcaagtggaa 3240  
 cgaaaaactca cgttaaggga ttttggctat gagattatca aaaaggatct tcacctagat 3300  
 ccttttaaat taaaaatgaa gttttaaatc aatctaaagt atatatgagt aaacttgggtc 3360  
 tgacagttac caatgcttaa tcagtggagg acctatctca gcgatctgtc tatttcgttc 3420  
 atccatagtt gctgactcc ccgtcgtgta gataactacg atacgggagg gcttaccatc 3480  
 tggccccagt gctgcaatga taccgcgaga cccacgctca ccggctccag atttatcagc 3540  
 aataaaccag ccagccggaa gggccgagcg cagaagtggg cctgcaactt tatccgcctc 3600  
 catccagtct attaatgtgt gccgggaagc tagagtaagt agttcgccag ttaatatgtt 3660  
 gcgcaacgtt gttgccattg ctacaggcat cgtgggtgca cgctcgtcgt ttggtatggc 3720  
 ttcattcagc tccggttccc aacgatcaag gcgagttaca tgatcccca tgttgtgcaa 3780  
 aaaagcgggt agctccttcg gtcctccgat cgttgtcaga agtaagttgg ccgcagtgtt 3840  
 atcaactcatg gttatggcag cactgcataa ttctcttact gtcatgccat ccgtaagatg 3900  
 cttttctgtg actggtgagt actcaaccaa gtcattctga gaatagtgtg tgcggcgacc 3960  
 gagttgctct tgccccggt caatacggga taataccgcy ccacatagca gaactttaaa 4020  
 agtgctcatc attgaaaaac gttcttcggg gcgaaaactc tcaaggatct taccgctgtt 4080  
 gagatccagt tcgatgtaac ccactcgtgc acccaactga tcttcagcat cttttacttt 4140  
 caccagcgtt tctgggtgag caaaaacagg aaggcaaaat gccgcaaaaa aggggaataag 4200  
 ggcgacacgg aaatgttgaa tactcatact cttccttttt caatattatt gaagcattta 4260  
 tcagggttat tgtctcatga gcggatacat atttgaatgt atttagaaaa ataaacaaat 4320  
 aggggttccg cgcacatttc cccgaaaagt gccacctgac gtctaagaaa ccattattat 4380  
 catgacatta acctataaaa ataggcgtat cagcaggccc tttcgtctcg cgcgtttcgg 4440  
 tgatgacggg gaaaacctct gacacatgca gctcccgag acggtcacag cttgtctgta 4500  
 agcggatgcc gggagcagac aagcccgtca gggcgctca gcgggtgttg gcgggtgtcg 4560  
 gggctggctt aactatgcgg catcagagca gattgtactg agagtgcacc atatggacat 4620  
 attgtcgta gaacgcggct acaattaata cataacctta tgtatcatac acatacgatt 4680  
 taggtgacac tata 4694

B10  
 cancelled